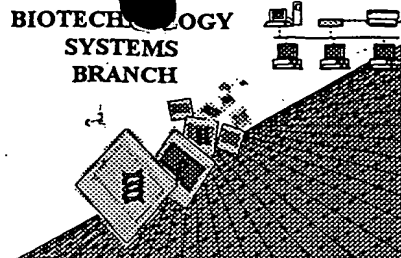


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/913,159

Source: PCT/09

Date Processed by STIC: 8/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

MAIL THIS COPY

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/913,159

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/913,159

DATE: 08/23/2001

TIME: 14:18:57

Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

Does Not Comply
Corrected Diskette Needed

5 <110> APPLICANT: Strathmann AG & Co.
 7 <120> TITLE OF INVENTION: Virus-Vaccine
 9 <130> FILE REFERENCE: P057760
 11 <140> CURRENT APPLICATION NUMBER: US/09/913,159
 12 <141> CURRENT FILING DATE: 2001-08-10
 14 <150> PRIOR APPLICATION NUMBER: 199 07 485.2
 15 <151> PRIOR FILING DATE: 1999-02-12
 17 <160> NUMBER OF SEQ ID NOS: 12
 19 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 9709
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Human immunodeficiency virus
 26 <400> SEQUENCE: 1

W--> 27 tggaagggt aatttggtcc caaaaaagac aagagatcct tgatctgtgg atctacca
 E--> 28 ca 60
 W--> 29 cacaaggcta ctccctgat tggcagaact acacaccagg gccagggatc aga
 E--> 30 tatccac 120
 W--> 31 tgaccttgg atggtgcttc aagttagtag cagttgaacc agagcaagta gaa
 E--> 32 gaggcca 180
 W--> 33 aataaggaga gaagaacagc ttgttacacc ctatgagcca gcatgggatg gag
 E--> 34 gacccgg 240
 E--> 35 agggagaagt attagtgtgg aagtttgaca gcctcctagc atttcgtcac
 E--> 36 atggcccag 300
 E--> 37 agctgcatcc ggagtactac aaagactgct gacatcgagc tttctacaag
 E--> 38 ggactttccg 360
 W--> 39 ctggggactt tccaggagg tgtggcctgg gcgggactgg ggagtggcga gccctca
 E--> 40 gat 420
 W--> 41 gctacatata agcagctgct ttttgctgt actgggtctc tctggttaga ccagatct
 E--> 42 ga 480
 E--> 43 gcctgggagc tctctggcta actaggaac ccactgctta agcctcaata
 E--> 44 aagcttgct 540
 W--> 45 tgagtgtca aagtagtgtg tgcccgtctg ttgtgtgact ctggttaacta ga
 E--> 46 gatccctc 600
 W--> 47 agaccctttt agtcagtgtg gaaaatctct agcagtggcg cccgaacagg gactt
 E--> 48 gaaag 660
 E--> 49 cgaaagtaaa gccagaggag atctctcgac gcaggactcg gcttgctgaa
 E--> 50 gcgcgcacgg 720
 W--> 51 caagaggcga ggggcggcga ctggtgagta cgccaaaaat tttgactagc ggaggcta
 E--> 52 ga 780
 W--> 53 aggagagaga tgggtgcgag agcgtcggt ttaagcggg gagaattaga taaf
 E--> 54 atgggaa 840
 W--> 55 aaaattcggg taaggccagg gggaaagaaa caatataaac taaaacatat ag

delete all dashes
move up

see
item 1
on Enov
summary
sheet

Per 1.822 of
Sequence Rules,
a maximum of
60 bases per line;
therefore, move bases
up

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/913,159

DATE: 08/23/2001

TIME: 14:18:57

Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

E--> 56 tatgggca 900
E--> 57 agcagggagc tagaacgatt cgcagttaat cctggccttt tagagacatc
E--> 58 agaaggctgt 960
W--> 59 agacaaatac tgggacagct acaaccatcc cttcagacag gatcagaaga acttagat-
E--> 60 ca 1020
W--> 61 ttatataata caatagcagt cctctattgt gtgcatcaaa ggatagatgt aaaaga-
E--> 62 cacc 1080
W--> 63 aaggaagcct tagataagat agaggaagag caaaacaaaa gtaagaaaaa ggcacag-
E--> 64 caa 1140
W--> 65 gcagcagctg acacaggaaa caacagccag gtcagccaaa attaccctat agtgca-
E--> 66 gaac 1200
E--> 67 ctccaggggc aaatggtaca tcaggccata tcacctagaa ctttaaatgc
E--> 68 atgggtaaaa 1260
W--> 69 gtagtagaag agaaggcttt cagcccagaa gtaataccca tgttttcagc attatca-
E--> 70 gaa 1320
W--> 71 ggagccaccc cacaagattt aaataccatg ctaaacacag tggggggaca tcaag-
E--> 72 cagcc 1380
E--> 73 atgcaaagt taaaagagac catcaatgag gaagctgcag aatgggatag
E--> 74 attgcatcca 1440
W--> 75 gtgcatgcag ggcctattgc accaggccag atgagagaac caaggggaag tgacatag-
E--> 76 ca 1500
E--> 77 ggaactacta gtacccttca ggaacaaata ggatggatga cacataatcc
E--> 78 acctatccca 1560
W--> 79 gtaggagaaa tctataaaag atggataatc ctgggattaa ataaaatagt aa-
E--> 80 gaatgtat 1620
W--> 81 agccctacca gcattctgga cataagacaa ggaccaaagg aaccctttag agac-
E--> 82 tatgta 1680
W--> 83 gaccgattct ataaaactct aagagccgag caagcttcac aagaggtaaa aa-
E--> 84 attggatg 1740
W--> 85 acagaaacct tgttggcca aaatgcgaac ccagattgta agactatttt aaaag-
E--> 86 cattg 1800
E--> 87 ggaccaggag cgacactaga agaaatgatg acagcatgtc agggagtggg
E--> 88 gggaccggc 1860
W--> 89 cataaagcaa gagttttggc tgaagcaatg agccaagtaa caaatccagc tacca-
E--> 90 taatg 1920
E--> 91 atacagaaag gcaattttag gaaccaaaga aagactgtta agtgtttcaa
E--> 92 ttgtggcaaa 1980
W--> 93 gaagggcaca tagccaaaaa ttgcagggcc cctaggaaaa agggctgttg gaa-
E--> 94 atgtgga 2040
W--> 95 aaggaaggac accaaatgaa agattgtact gagagacagg ctaatttttt agggaa-
E--> 96 gac 2100
W--> 97 tggccttccc acaaggggaag gccaggggaat tttcttcaga gcagaccaga gccaa-
E--> 98 cagcc 2160
W--> 99 ccaccagaag agagcttcag gtttggggaa gagacaacaa ctccctctca gaagcag-
E--> 100 gag 2220
E--> 101 ccgatagaca aggaactgta tccttttagct tccctcagat cactctttgg
E--> 102 cagcgacccc 2280
W--> 103 tcgtcacaat aaagataggg gggcaattaa aggaagctct attagatata ggagca-
E--> 104 gatg 2340

*same
errors*

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/913,159

TIME: 14:18:57

Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

E--> 105 atacagtatt agaagaaatg aatttgccag gaagatggaa accaaaaatg
 E--> 106 atagggggaa 2400
 W--> 107 ttggagggtt tatcaaagta ggacagtatg atcagatact catagaaatc tgcggaca-
 E--> 108 ta 2460
 W--> 109 aagctatagg tacagtatta gtaggacctt cacctgtcaa cataattgga agaa-
 E--> 110 atctgt 2520
 W--> 111 tgactcagat tggctgcact ttaaattttc ccattagtcc tattgagact gtaccag-
 E--> 112 taa 2580
 W--> 113 aattaaagcc aggaatggat ggcccaaaag ttaaacaatg gccattgaca gaagaa-
 E--> 114 aaaa 2640
 W--> 115 taaaagcatt agtagaaatt tgtacagaaa tggaaaagga aggaaaaatt tcaaaa-
 E--> 116 attg 2700
 W--> 117 ggcttgaaaa tccatacaat actccagtat ttgccataaa gaaaaaagac agtactaa-
 E--> 118 at 2760
 E--> 119 ggagaaaaatt agtagatttc agagaactta ataagagaac tcaagatttc
 E--> 120 tgggaagtgc 2820
 E--> 121 aattaggaat accacatcct gcagggttaa aacagaaaaa atcagtaaca
 E--> 122 gtactggatg 2880
 W--> 123 tgggcgatgc atatttttca gttcccttag ataaagactt caggaagtat actgcatt-
 E--> 124 ta 2940
 E--> 125 ccataccatg tataaacaat gagacaccag ggattagata tcagtacaat
 E--> 126 gtgcttcac 3000
 W--> 127 agggatggaa aggatcacca gcaatattcc agtgtagcat gacaaaaatc tta-
 E--> 128 gagcctt 3060
 W--> 129 ttagaaaaa aaatccagac atagtcact atcaatacat ggatgatttg tatgtag-
 E--> 130 gat 3120
 W--> 131 ctgacttaga aatagggcag catagaacaa aaatagagga actgagacaa catctgtt-
 E--> 132 ga 3180
 E--> 133 ggtggggatt taccacacca gacaaaaaac atcagaaaga acctccattc
 E--> 134 ctttgatgg 3240
 W--> 135 gttatgaact ccatcctgat aaatggacag tacagcctat agtgctgcca gaaaagga-
 E--> 136 ca 3300
 W--> 137 gctggactgt caatgacata cagaaattag tgggaaaatt gaattgggca agtca-
 E--> 138 gattt 3360
 W--> 139 atgcagggat taaagtaagg caattatgta aacttcttag gggaaccaa gcactaa-
 E--> 140 cag 3420
 W--> 141 aagtagtacc actaacagaa gaagcagagc tagaactggc agaaaacagg ga-
 E--> 142 gattctaa 3480
 W--> 143 aagaaccggg acatggagtg tattatgacc catcaaaaga cttaatagca gaaataca-
 E--> 144 ga 3540
 W--> 145 agcaggggca aggccaatgg acatatcaaa tttatcaaga gccatttaaa aatct-
 E--> 146 gaaaa 3600
 W--> 147 caggaaaata tgcaagaatg aagggtgccc aactaatga tgtgaaacaa ttaaca-
 E--> 148 gagg 3660
 W--> 149 cagtacaaaa aatagccaca gaaagcatag taatatgggg aaagactcct aaatt-
 E--> 150 taaat 3720
 E--> 151 taccatata aaaggaaaca tgggaagcat ggtggacaga gtattggcaa
 E--> 152 gccacctgga 3780
 W--> 153 ttcctgagtg ggagtttgtc aatacccctc ccttagtgaa gttatggtac cagttaga-

Same

RAW SEQUENCE LISTING

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TIME: 14:18:57

Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

E--> 154 ga 3840
 W--> 155 aagaacccat aataggagca gaaactttct atgtagatgg ggcagccaat agggaa-
 E--> 156 acta 3900
 E--> 157 aattaggaaa agcaggatat gtaactgaca gaggaagaca aaaagttgtc
 E--> 158 cccctaacgg 3960
 E--> 159 acacaacaaa tcagaagact gagttacaag caattcatct agctttgcag
 E--> 160 gattcgggat 4020
 W--> 161 tagaagtaa catagtga gactcacaat atgcattggg aatcattcaa gcacaac-
 E--> 162 cag 4080
 W--> 163 ataagagtga atcagagtta gtcagtcaaa taatagagca gttaataaaa aaggaa-
 E--> 164 aaag 4140
 W--> 165 tctacctggc atgggtacca gcacacaaag gaattggagg aatgaacaa gta-
 E--> 166 gatgggt 4200
 W--> 167 tggtcagtgc tggaatcagg aaagtactat ttttagatgg aatagataag gcccaa-
 E--> 168 gaag 4260
 W--> 169 aacatgagaa atatcacagt aattggagag caatggctag tgattttaac ctac-
 E--> 170 cacctg 4320
 E--> 171 tagtagcaaa agaaatagta gccagctgtg ataaatgtca gctaaaaggg
 E--> 172 gaagccatgc 4380
 W--> 173 atggacaagt agactgtagc ccaggaatat ggcagctaga ttgtacacat ttagaag-
 E--> 174 gaa 4440
 E--> 175 aagttatctt ggtagcagtt catgtagcca gtggatatat agaagcagaa
 E--> 176 gtaattccag 4500
 W--> 177 cagagacagg gcaagaaaca gcatacttcc tcttaaaatt agcaggaaga tggccag-
 E--> 178 taa 4560
 E--> 179 aaacagtaca tacagacaat ggcagcaatt tcaccagtac tacagttaag
 E--> 180 gccgcctgtt 4620
 W--> 181 ggtgggaggg gatcaagcag gaatttggca ttccctacaa tccccaaagt caaggag-
 E--> 182 taa 4680
 W--> 183 tagaatctat gaataaagaa ttaaagaaaa ttataggaca ggtaagagat caggct-
 E--> 184 gaac 4740
 W--> 185 atcttaagac agcagtacaa atggcagtat tcatccacaa ttttaaaaga aa-
 E--> 186 agggggga 4800
 W--> 187 ttggggggta cagtgcaggg gaaagaatag tagacataat agcaacagac atacaa-
 E--> 188 acta 4860
 W--> 189 aagaattaca aaaacaaatt acaaaaattc aaaattttcg ggtttattac agggacag-
 E--> 190 ca 4920
 W--> 191 gagatccagt ttggaaagga ccagcaaagc tcctctggaa aggtgaaggg gcagtag-
 E--> 192 taa 4980
 W--> 193 tacaagataa tagtgacata aaagtagtgc caagaagaaa agcaaagatc at-
 E--> 194 cagggatt 5040
 W--> 195 atggaaaaca gatggcaggg gatgattgtg tggcaagtag acaggatgag gattaa-
 E--> 196 caca 5100
 E--> 197 tggaaaagat tagtaaaaca ccatatgtat atttcaagga aagctaagga
 E--> 198 ctgggtttat 5160
 W--> 199 agacatcact atgaaagtac taatccaaaa ataagttcag aagtacacat cccac-
 E--> 200 taggg 5220
 E--> 201 gatgctaaat tagtaataac aacatattgg ggtctgcata caggagaaag
 E--> 202 agactggcat 5280

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/913,159

DATE: 08/23/2001

TIME: 14:18:57

Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

W--> 203 ttgggtcagg gagtctccat agaattggagg aaaaagagat atagcacaca agta-
E--> 204 gacct 5340
W--> 205 gacctagcag accaactaat tcattctgcac ttttttgatt gtttttcaga atctgcta-
E--> 206 ta 5400
W--> 207 agaaatacca tattaggacg tatagttagt cctaggtgtg aatatcaagc aggaca-
E--> 208 taac 5460
W--> 209 aaggtaggat ctctacagta cttggcacta gcagcattaa taaaaccaa acagataa-
E--> 210 ag 5520
W--> 211 ccacctttgc ctagtgttag gaaactgaca gaggacagat ggaacaagcc ccagaa-
E--> 212 gacc 5580
W--> 213 aagggccaca gagggagcca tacaatgaat ggacactaga gcttttagag gaacttaa-
E--> 214 ga 5640
W--> 215 gtgaagctgt tagacatttt cctaggatat ggctccataa cttaggacaa ca-
E--> 216 tatctatg 5700
W--> 217 aaacttacgg ggatacttgg gcaggagtgg aagccataat aagaattctg caa-
E--> 218 caactgc 5760
W--> 219 tgtttatcca ttccagaatt ggggtgtcgac atagcagaat aggcgttact cgacagag-
E--> 220 ga 5820
W--> 221 gagcaagaaa tggagccagt agatcctaga ctagagccct ggaagcatcc aggaagt-
E--> 222 cag 5880
E--> 223 cctaaaactg cttgtaccaa ttgctattgt aaaaagtgtt gctttcattg
E--> 224 ccaagtttgt 5940
W--> 225 ttcattgaaa aagccttagg catctcctat ggcaggaaga agcggagaca gcgacgaa-
E--> 226 ga 6000
W--> 227 gctcatcaga acagtcagac tcattcaagct tctctatcaa agcagtaagt agta-
E--> 228 catgta 6060
W--> 229 atgcaaccta taatagtagc aatagtagca ttagtagtag caataataat agcaa-
E--> 230 tagtt 6120
W--> 231 gtgtggtcca tagtaatcat agaattatagg aaaatattaa gacaaagaaa aataga-
E--> 232 cagg 6180
W--> 233 ttaattgata gactaataga aagagcagaa gacagtggca atgagagtga aggagaag-
E--> 234 ta 6240
W--> 235 tcagcacttg tggagatggg ggtggaaatg gggcaccatg ctcttggga tattgat-
E--> 236 gat 6300
W--> 237 ctgtagtgct acagaaaaat tgtgggtcac agtctattat ggggtacctg tgtggaag-
E--> 238 ga 6360
W--> 239 agcaaccacc actctatttt gtgcatcaga tgctaaagca tatgatacag aggtaca-
E--> 240 taa 6420
W--> 241 tgtttgggcc acacatgcct gtgtacccac agaccccaac ccacaagaag tag-
E--> 242 tattggt 6480
W--> 243 aatgtgaca gaaaatttta acatgtggaa aatgacatg gtagaacaga tgcattgag-
E--> 244 ga 6540
E--> 245 tataatcagt ttatgggatc aaagcctaaa gccatgtgta aaattaaccc
E--> 246 cactctgtgt 6600
W--> 247 tagtttaag tgactgatt tgaagaatga tactaatacc aatagtagta gcggga-
E--> 248 gaat 6660
W--> 249 gataatggag aaaggagaga taaaaaactg ctctttcaat atcagcacia gcataa-
E--> 250 gaga 6720
W--> 251 taaggtgcag aaagaatatg cattctttta taaacttgat atagtaccaa tagataa-

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DATE: 08/23/2001

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Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

E--> 252 tac 6780
 W--> 253 cagctatagg ttgataagtt gtaacacctc agtcattaca caggcctgtc caa-
 E--> 254 aggtatc 6840
 W--> 255 ctttgagcca attcccatac attattgtgc cccggctggt tttgcgattc taa-
 E--> 256 aatgtaa 6900
 W--> 257 taataagacg ttcaatggaa caggaccatg tacaaatgtc agcacagtac aatgtaca-
 E--> 258 ca 6960
 W--> 259 tggaatcagg ccagtagtat caactcaact gctgttaaat ggcagtctag cagaa-
 E--> 260 gaaga 7020
 W--> 261 tgtagtaatt agatctgcc aatttcacaga caatgctaaa accataatag tacagct-
 E--> 262 gaa 7080
 E--> 263 cacatctgta gaaattaatt gtacaagacc caacaacaat acaagaaaaa
 E--> 264 gtatccgtat 7140
 W--> 265 ccagagggga ccagggagag cttttgttac aataggaaaa ataggaaata tgaga-
 E--> 266 caagc 7200
 W--> 267 acattgtaac attagtagag caaaatggaa tgccacttta aacagatag ctagcaa-
 E--> 268 att 7260
 E--> 269 aagagaacaa tttggaaata ataaaacaat aatctttaag caatcctcag
 E--> 270 gaggggaccc 7320
 W--> 271 agaaattgta acgcacagtt ttaattgttg aggggaattt ttctactgta attcaa-
 E--> 272 caca 7380
 W--> 273 actgtttaat agtacttgggt ttaatagtag ttggagtact gaaggggtcaa ataact-
 E--> 274 ga 7440
 W--> 275 aggaagtgc acaatcacac tcccatgcag aataaaacaa tttataaaca tgtggcag-
 E--> 276 ga 7500
 W--> 277 agtaggaaaa gcaatgtatg cccctcccat cagtggacaa attagatgtt catcaaa-
 E--> 278 tat 7560
 W--> 279 tactgggctg ctattaacaa gagatgggtg taataacaac aatgggtccg agatctt-
 E--> 280 cag 7620
 W--> 281 acctggagga ggcgatatga gggacaattg gagaagtga ttatataaat ataaag-
 E--> 282 tagt 7680
 W--> 283 aaaaattgaa ccattaggag tagcaccac caaggcaaag agaagagtgg tgcagaga-
 E--> 284 ga 7740
 W--> 285 aaaaagagca gtgggaatag gagctttgtt cttggggttc ttgggagcag caggaag-
 E--> 286 cac 7800
 W--> 287 tatgggctgc acgtcaatga cgctgacggt acaggccaga caattattgt ctgata-
 E--> 288 tagt 7860
 W--> 289 gcagcagcag aacaatttgc tgagggctat tgaggcgcaa cagcatctgt tgcaact-
 E--> 290 cac 7920
 W--> 291 agtctggggc atcaaacagc tccaggcaag aatcctgggt gtggaaagat acctaa-
 E--> 292 agga 7980
 E--> 293 tcaacagctc ctggggattt ggggttgctc tggaaaactc atttgcacca
 E--> 294 ctgctgtgcc 8040
 E--> 295 ttggaatgct agttggagta ataaatctct ggaacagatt tgggaataaca
 E--> 296 tgacctggat 8100
 W--> 297 ggagtgggac agagaaatta acaattacac aagcttaata cactccttaa ttgaa-
 E--> 298 gaac 8160
 E--> 299 gcaaaaccag caagaaaaga atgaacaaga attattggaa ttagataaat
 E--> 300 gggcaagttt 8220

same

RAW SEQUENCE LISTING
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Input Set : A:\P057760.app
 Output Set: N:\CRF3\08162001\I913159.raw

W--> 301 gtggaattgg tttaacataa caaattggct gtggtatata aaattattca taatga-
 E--> 302 tagt 8280
 W--> 303 aggaggcttg gtaggtttta gaatagtttt tgctgtactt tctatagtga atagagt-
 E--> 304 tag 8340
 W--> 305 gcagggatat tcaccattat cgtttcagac ccacctccca atcccaggagg gacccga-
 E--> 306 cag 8400
 W--> 307 gcccgaagga atagaagaag aaggtggaga gagagacaga gacagatcca ttcgat-
 E--> 308 tagt 8460
 W--> 309 gaacggatcc ttagcactta tctgggacga tctgcgagc ctgtgcctct tcagctac-
 E--> 310 ca 8520
 E--> 311 ccgcttgaga gacttactct tgattgtaac gaggattgtg gaacttctgg
 E--> 312 gacgcagggg 8580
 W--> 313 gtgggaagcc ctcaaattt ggtggaatct cctacagtat tggagtcagg aactaaa-
 E--> 314 gaa 8640
 W--> 315 tagtgctgtt aacttgctca atgccacagc catagcagta gctgagggga caga-
 E--> 316 taggg 8700
 W--> 317 tatagaagta ttacaagcag cttatagagc tattcgccac atacctagaa gaataa-
 E--> 318 gaca 8760
 W--> 319 gggcttgaa aggattttgc tataagatgg gtggcaagt gtcaaaaagt agtgt-
 E--> 320 gattg 8820
 E--> 321 gatggcctgc tgtaaggga agaattgagc gagctgagcc agcagcagat
 E--> 322 ggggtgggag 8880
 W--> 323 cagtatctcg agacctagaa aaacatggag caatcacaag tagcaatata gcagctaa-
 E--> 324 ca 8940
 W--> 325 atgctgcttg tgcttgcta gaagcacaag aggaggaaga ggtgggtttt ccagtca-
 E--> 326 cac 9000
 W--> 327 ctcaggatcc tttaagacca atgacttaca aggcagctgt agatcttagc cactttt-
 E--> 328 taa 9060
 W--> 329 aagaaaaggg gggactggaa gggctaattc actcccaaag aagacaagat atcctt-
 E--> 330 gatc 9120
 E--> 331 tgtggatcta ccacacacaa ggctacttcc ctgattggca gaactacaca
 E--> 332 ccagggccag 9180
 W--> 333 gggctagata tccactgacc tttggatggg gctacaagct agtaccagtt gagccaga-
 E--> 334 ta 9240
 E--> 335 aggtagaaga ggccaataaa ggagagaaca ccagcttggt acaccctgtg
 E--> 336 agcctgcatg 9300
 W--> 337 gaatggatga ccctgagaga gaagtgttag agtggagggt tgacagccgc ctag-
 E--> 338 catttc 9360
 E--> 339 atcacgtggc ccgagagctg catccggagt acttcaagaa ctgctgacat
 E--> 340 cgagcttgct 9420
 E--> 341 acaagggact ttccgctggg gactttccag ggaggcgtgg cctgggcggg
 E--> 342 actggggagt 9480
 E--> 343 ggcgagccct cagatgctgc atataagcag ctgctttttg cctgtactgg
 E--> 344 gtctctctgg 9540
 E--> 345 ttagaccaga tctgagcctg ggagctctct ggctaactag ggaaccact
 E--> 346 gcttaagcct 9600
 E--> 347 caataaagct tgccttgagt gcttcaagta gtgtgtgccc gtctgttgtg
 E--> 348 tgactctgg 9660
 E--> 349 aactagagat ccctcagacc cttttagtca gtgtggaaaa tctctagca

Same

RAW SEQUENCE LISTING
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Input Set : A:\P057760.app
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E--> 350 9709
633 <210> SEQ ID NO: 3
634 <211> LENGTH: 107
635 <212> TYPE: DNA
636 <213> ORGANISM: Artificial Sequence
638 <220> FEATURE:
639 <223> OTHER INFORMATION: Description of the artificial sequence:
640 oligonucleotide for cloning
642 <400> SEQUENCE: 3
W--> 643 aagatgtagt aattagatct gccaatctca cagacaatgc taaaaccata atagta- *same*
E--> 644 cagc 60
E--> 645 tgaacacatc gttagaaatt aattgtacaa gacccaacaa caataca
E--> 646 107
649 <210> SEQ ID NO: 4
650 <211> LENGTH: 120
651 <212> TYPE: DNA
652 <213> ORGANISM: Artificial Sequence
654 <220> FEATURE:
655 <223> OTHER INFORMATION: Description of the artificial sequence:
656 oligonucleotide for cloning
658 <220> FEATURE:
659 <221> NAME/KEY: misc_feature
660 <222> LOCATION: (97)..(99)
661 <223> OTHER INFORMATION: Sequence at this position: (GA)(AT)(GATC), ie.
662 base at position 97 can be G or A, base at
663 position 98 can be A or T, and base at
664 position 99 can be G, A, T or C.
666 <400> SEQUENCE: 4
E--> 667 ttttgcctcta gaaatgttac aatgtgcttg tcttatgtct cctgttgtag
668 cttctgttgc 60
E--> 669 atgaaatgct ctccctgggc cgatatggat actatgrwnt tttcttgc
670 tgttggtggg 120
673 <210> SEQ ID NO: 5
674 <211> LENGTH: 17
675 <212> TYPE: DNA
676 <213> ORGANISM: Artificial Sequence
678 <220> FEATURE:
679 <223> OTHER INFORMATION: Description of the artificial sequence:
680 sequencing primer
682 <400> SEQUENCE: 5
E--> 683 ccatgtacaa atgtcag
684 17
687 <210> SEQ ID NO: 6
688 <211> LENGTH: 17
689 <212> TYPE: DNA
690 <213> ORGANISM: Artificial Sequence
692 <220> FEATURE:
693 <223> OTHER INFORMATION: Description of the artificial sequence:
694 sequencing primer *same*

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Input Set : A:\P057760.app
Output Set: N:\CRF3\08162001\I913159.raw

696 <400> SEQUENCE: 6
E--> 697 aaaactgtgc gttacaa
698 17
701 <210> SEQ ID NO: 7
702 <211> LENGTH: 17
703 <212> TYPE: DNA
704 <213> ORGANISM: Artificial Sequence
706 <220> FEATURE:
707 <223> OTHER INFORMATION: Description of the artificial sequence:
708 sequencing primer
710 <400> SEQUENCE: 7
E--> 711 gtaaaacgac ggccagt
712 17
715 <210> SEQ ID NO: 8
716 <211> LENGTH: 17
717 <212> TYPE: DNA
718 <213> ORGANISM: Artificial Sequence
720 <220> FEATURE:
721 <223> OTHER INFORMATION: Description of the artificial sequence:
722 sequencing primer
724 <400> SEQUENCE: 8
E--> 725 caggaaacag ctatgac
726 17
729 <210> SEQ ID NO: 9
730 <211> LENGTH: 2148
731 <212> TYPE: DNA
732 <213> ORGANISM: Artificial Sequence
734 <220> FEATURE:
735 <223> OTHER INFORMATION: Description of the artificial sequence: synthetic DNA
737 <220> FEATURE:
738 <221> NAME/KEY: misc_feature
739 <222> LOCATION: (3)..(9)
740 <223> OTHER INFORMATION: BstEII cleavage site
742 <220> FEATURE:
743 <221> NAME/KEY: misc_feature
744 <222> LOCATION: (2143)..(2148)
745 <223> OTHER INFORMATION: BamHI cleavage site
747 <400> SEQUENCE: 9
E--> 748 tgggtcaccg tctattatgg ggtgcctgtg tggaaggaag caaccaccac
749 tctattttgt 60
E--> 750 gcatcagatg ctaaagcata tgatacagag gtacataatg tttgggccac
751 acatgcctgt 120
W--> 752 gtaccacag accccaaccc acaagaagta gtattggtaa atgtgacaga aaattt-
E--> 753 taac 180
W--> 754 atgtggaaaa atgacatggt agaacagatg catgaggata taatcagttt atgggat-
E--> 755 caa 240
W--> 756 agccttaagc catgtgtaaa attaacccca ctctgtgtta gtttaaagtg cact-
E--> 757 gatttg 300
W--> 758 aagaatgata ctaataccaa tagtagtagc gggagaatga taatggagaa aggagaga-

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Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

E--> 759 ta 360
 W--> 760 aaaaactgca gcttcaatat cagcacaagc ataagagata aggtgcagaa agaa-
 E--> 761 tatgca 420
 W--> 762 ttcttttata aacttgatat agtaccata gataatacca gctataggtt ga-
 E--> 763 taagttgt 480
 W--> 764 aacacctcag tgatcacaca ggcctgtcca aaggtatcct ttgagccaat tcccata-
 E--> 765 cat 540
 W--> 766 tattgtgccc cggctggttt tgcgattcta aaatgtaata ataagacgtt caatggaa-
 E--> 767 ca 600
 W--> 768 ggaccatgta caaatgtcag cacagtacaa tgtacacatg gaattcgacc agtagtat-
 E--> 769 ca 660
 E--> 770 actcaactgc tgttaaatgg cagtctagca gaagaagatg tagtaattag
 E--> 771 atctgccaat 720
 W--> 772 ttcacagaca atgctaaaac cataatagta cagctgaaca catctgtaga aat-
 E--> 773 taattgt 780
 W--> 774 acaagacca acaacaatac aagaaaaagt atccgtatcc agaggggacc agggagag-
 E--> 775 ca 840
 W--> 776 tttgttacaa taggaaaaat aggaaatatg agacaagcac attgtaacat ttctagag-
 E--> 777 ca 900
 W--> 778 aatggaatg ccacttttaa acagatagct agcaaattaa gagaacaatt tggaaa-
 E--> 779 taat 960
 W--> 780 aaaacaataa tctttaagca gtcatccgga ggggaccag aaattgtaac gca-
 E--> 781 cagtttt 1020
 E--> 782 aattgtggag gggaattttt ctactgtaat tcaacacaac tgtttaatag
 E--> 783 tacttggttt 1080
 W--> 784 aatagtactt ggagtactga aggttcaa aacactgaag gaagtgcac aatca-
 E--> 785 cactc 1140
 E--> 786 ccattgcagaa taaaacaatt tataaacatg tggcaggaag taggaaaagc
 E--> 787 aatgtatgcc 1200
 W--> 788 cctcccatca gtggccaaat tagatgttca tcaaataatta ctgggctgct at-
 E--> 789 taactcga 1260
 W--> 790 gatggtggtg ataacaacaa tgggtccgag attttcagac ctggaggagg cgatat-
 E--> 791 gagg 1320
 W--> 792 gataattgga gaagtgaatt atataaatat aaagtagtaa aaattgaacc attaggag-
 E--> 793 ta 1380
 W--> 794 gcacccacca aggcaaagag acgcgtggtg cagagagaaa agcgcgcagt gggaa-
 E--> 795 tagga 1440
 W--> 796 gctctgttcc ttgggttctt gggagcagca ggaagcacta tgggcgcagc gtcaat-
 E--> 797 gacg 1500
 E--> 798 ctgacggtac aggccagaca attattgtct gatatagtgc agcagcagaa
 E--> 799 caatttgctg 1560
 W--> 800 agggcaattg aggcgcaaca gcattctgtt caactcacag tctggggcat caaa-
 E--> 801 cagctc 1620
 E--> 802 caggcaagaa tcttggtgtg ggaaagatac ctaaaggatc aacagctcct
 E--> 803 ggggatttgg 1680
 W--> 804 ggttgctctg gaaaactcat ttgcaccact gctgtgcctt ggaatgctag ttggag-
 E--> 805 taat 1740
 W--> 806 aaatctctgg aacagatttg gaataacatg acctggatgg agtgggacag agaaat-
 E--> 807 taac 1800

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Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

W--> 808 aattacacaa gcttaataca ctccttaatt gaagaatcgc aaaaccagca agaaaa-
 E--> 809 gaat 1860
 W--> 810 gaacaagaat tattggaatt agataaatgg gcaagtttgt ggaattgggt taacataa-
 E--> 811 ca 1920
 W--> 812 aattggctgt ggtatataaa attattcata atgatagtag gaggcttggt aggtt-
 E--> 813 taaga 1980
 W--> 814 atagtttttg ctgtactttc tatagtgaat agagttaggc agggatattc accat-
 E--> 815 tatcg 2040
 W--> 816 tttcagaccc acctcccaat cccgagggga cccgacaggc ccgaaggaat agaagaa-
 E--> 817 gaa 2100
 E--> 818 ggtggagaga gagacagaga cagatccatt cgattagtga acggatcc
 E--> 819 2148
 822 <210> SEQ ID NO: 10
 823 <211> LENGTH: 6229
 824 <212> TYPE: DNA
 825 <213> ORGANISM: Artificial Sequence
 827 <220> FEATURE:
 828 <223> OTHER INFORMATION: Description of the artificial sequence: synthetic DNA
 830 <220> FEATURE:
 831 <221> NAME/KEY: sig_peptide
 832 <222> LOCATION: (1293)..(1295)
 833 <223> OTHER INFORMATION: env ATG
 835 <220> FEATURE:
 836 <221> NAME/KEY: misc_feature
 837 <222> LOCATION: (1377)..(1379)
 838 <223> OTHER INFORMATION: env AGT, gp120 start
 840 <220> FEATURE:
 841 <221> NAME/KEY: misc_feature
 842 <222> LOCATION: (1397)..(1403)
 843 <223> OTHER INFORMATION: BstEII cleavage site
 845 <220> FEATURE:
 846 <221> NAME/KEY: misc_feature
 847 <222> LOCATION: (3537)..(3542)
 848 <223> OTHER INFORMATION: BamHI cleavage site
 850 <220> FEATURE:
 851 <221> NAME/KEY: misc_feature
 852 <222> LOCATION: (3855)..(3857)
 853 <223> OTHER INFORMATION: env TAA, stop
 855 <400> SEQUENCE: 10
 W--> 856 ctgacgcgcc ctgtagcggc gcattaagcg cggcggtgt ggtggttacg cgcagcgt-
 E--> 857 ga 60
 E--> 858 ccgtacact tgccagcgcc cttagcggcg ctcctttcgc tttcttcct
 E--> 859 tcctttctcg 120
 E--> 860 ccacgttcgc cggtttccc cgtcaagctc taaatcgggg gctcccttta
 E--> 861 gggttccgat 180
 E--> 862 ttagtgcttt acggcacctc gaccccaaaa aacttgatta gggatgatgt
 E--> 863 tcacgtagt 240
 W--> 864 ggcacgcgcc ctgatagacg gtttttcgcc ctttgacgtt ggagtccacg ttcttta-
 E--> 865 ta 300

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Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

E--> 866 gtggactctt gttccaaact ggaacaacac tcaaccctat ctcggtctat
E--> 867 tcttttgatt 360
W--> 868 tataagggat tttgccgatt tcggcctatt ggttaaaaaa tgagctgatt taacaa-
E--> 869 aaat 420
E--> 870 ttaacgcgaa ttttaacaaa atattaacgc ttacaatttc cattcgccat
E--> 871 tcaggctgcg 480
W--> 872 caactgttgg gaagggcgat cgggtgcgggc ctcttcgcta ttacgccagc tggcgaa-
E--> 873 agg 540
W--> 874 gggatgtgct gcaaggcgat taagttgggt aacgccaggg ttttcccagt cac-
E--> 875 gacgttg 600
W--> 876 taaaacgacg gccagtgagc gtctagttat taatagtaat caattacggg gtcac-
E--> 877 tagtt 660
E--> 878 catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc
E--> 879 gcctggctga 720
W--> 880 ccgcccacg acccccgccc attgacgtca ataatgacgt atgttcccat ag-
E--> 881 taacgcca 780
E--> 882 atagggactt tccattgacg tcaatgggtg gagtatattac ggtaaactgc
E--> 883 ccacttgga 840
W--> 884 gtacatcaag tgtatcatat gccaaagtacg cccctattg acgtcaatga cggtaa-
E--> 885 atgg 900
W--> 886 ccgcctggc attatgccc gtacatgacc ttatgggact ttcctacttg gcagta-
E--> 887 catc 960
E--> 888 tacgtattag tcatcgctat taccatgggtg atgcggtttt ggcagtacat
E--> 889 caatgggct 1020
E--> 890 ggatagcggg ttgactcacg gggatttcca agtctccacc ccattgacgt
E--> 891 caatgggagt 1080
E--> 892 ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaacaactc
E--> 893 cgccccattg 1140
E--> 894 acgcaaatgg gcggtaggcg tgtacgggtg gaggtctata taagcagagc
E--> 895 tcgttttagtg 1200
W--> 896 aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag aaga-
E--> 897 caccgg 1260
W--> 898 gacaattcga gtcgggtacc gtcgacgcca ccatgagagt gaaggagaag tatcag-
E--> 899 cact 1320
E--> 900 tgtggagatg ggggtggaaa tggggcacca tgctccttg gatattgatg
E--> 901 atctgtagt 1380
W--> 902 ctacagaaaa attgtgggtc accgtctatt atgggggtacc tgtgtggaag gaagcaac-
E--> 903 ca 1440
E--> 904 ccactctatt ttgtgcatca gatgctaaag catatgatac agagggtacat
E--> 905 aatgtttggg 1500
W--> 906 ccacacatgc ctgtgtaccc acagacccca acccacaaga agtagtattg gtaaagt-
E--> 907 ga 1560
W--> 908 cagaaaattt taacatgtgg aaaaatgaca tggtagaaca gatgcatgag gatataat-
E--> 909 ca 1620
W--> 910 gtttatggga tcaaagccta aagccatgtg taaaattaac cccactctgt gttagtt-
E--> 911 taa 1680
W--> 912 agtgcactga tttgaagaat gatactaata ccaatagtag tagcgggaga atga-
E--> 913 taatgg 1740
W--> 914 agaaaggaga gataaaaaac tgctctttca atatcagcac aagcataaga ga-

Same

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Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

E--> 915 taaggtgc 1800
W--> 916 agaaagaata tgcattcttt tataaacttg atatagtacc aatagataat accagcta-
E--> 917 ta 1860
E--> 918 ggttgataag ttgtaacacc tcagtcatta cacaggcctg tccaaaggta
E--> 919 tcctttgagc 1920
W--> 920 caattcccat acattattgt gccccggctg gttttgcgat tctaaaatgt aataa-
E--> 921 taaga 1980
W--> 922 cgttcaatgg aacaggacca tgtacaaatg tcagcacagt acaatgtaca catggaat-
E--> 923 ca 2040
W--> 924 ggccagtagt atcaactcaa ctgctgttaa atggcagtct agcagaagaa gatgtag-
E--> 925 taa 2100
W--> 926 ttagatctgc caatttcaca gacaatgcta aaaccataat agtacagctg aaca-
E--> 927 catctg 2160
W--> 928 tagaaattaa ttgtacaaga cccaacaaca atacaagaaa aagtatccgt atcca-
E--> 929 gaggg 2220
W--> 930 gaccagggag agcatttgtt acaataggaa aaataggaaa tatgagacaa gca-
E--> 931 cattgta 2280
W--> 932 acattagtag agcaaaatgg aatgccactt taaaacagat agctagcaaa ttaaga-
E--> 933 gaac 2340
W--> 934 aatttggaag taataaaaca ataacttcta agcaatcctc aggaggggac ccagaa-
E--> 935 attg 2400
W--> 936 taacgcacag ttttaattgt ggaggggaat ttttctactg taattcaaca caactgtt-
E--> 937 ta 2460
W--> 938 atagtacttg gtttaatagt acttgaggta ctgaagggtc aaataacact gaag-
E--> 939 gaagtg 2520
W--> 940 acacaatcac actcccatgc agaataaaac aatttataaa catgtggcag gaagtag-
E--> 941 gaa 2580
W--> 942 aagcaatgta tgcccctccc atcagtggac aaattagatg ttcacaaat at-
E--> 943 tactgggc 2640
E--> 944 tgctattaac aagagatggt ggtaataaca acaatgggtc cgagatcttc
E--> 945 agacctggag 2700
W--> 946 gaggcgatat gagggacaat tggagaagtg aattatataa atataaagta gtaaaa-
E--> 947 attg 2760
W--> 948 aaccattagg agtagcacc accaaggcaa agagaagagt ggtgcagaga gaaaaaa-
E--> 949 gag 2820
W--> 950 cagtgggaat aggagctttg ttccttgggt tcttgggagc agcaggaagc ac-
E--> 951 tatgggct 2880
W--> 952 gcacgtcaat gacgtgacg gtacaggcca gacaattatt gtctgatata gtgcag-
E--> 953 cagc 2940
E--> 954 agaacaattt gctgagggct attgaggcgc aacagcatct gttgcaactc
E--> 955 acagtctggg 3000
W--> 956 gcatcaaaca gctccaggca agaatcctgg ctgtggaaag atacctaaag gatcaa-
E--> 957 cagc 3060
E--> 958 tcctggggat ttgggggtgc tctggaaaac tcatttgac cactgctgtg
E--> 959 ccttggaatg 3120
E--> 960 ctagtggag taataaatct ctggaacaga tttggaataa catgacctg
E--> 961 atggagtggg 3180
W--> 962 acagagaaat taacaattac acaagcttaa tacactcctt aattgaagaa tcgcaa-
E--> 963 aacc 3240

same

RAW SEQUENCE LISTING

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Input Set : A:\P057760.app

Output Set: N:\CRF3\08162001\I913159.raw

E--> 964 agcaagaaaa gaatgaacaa gaattattgg aattagataa atgggcaagt
 E--> 965 ttgtggaatt 3300
 W--> 966 ggtttaacat aacaaattgg ctgtggtata taaaattatt cataatgata gtag-
 E--> 967 gaggt 3360
 E--> 968 tggtaggttt aagaatagtt tttgctgtac tttctatagt gaatagagtt
 E--> 969 aggcagggat 3420
 E--> 970 attcaccatt atcgtttcag acccacctcc caatcccgag gggacccgac
 E--> 971 aggcccgag 3480
 E--> 972 gaatagaaga agaaggtgga gagagagaca gagacagatc cattcgatta
 E--> 973 gtgaacggat 3540
 W--> 974 ccttagcact tatctgggac gatctgcgga gcctgtgcct cttcagctac caccgctt-
 E--> 975 ga 3600
 E--> 976 gagacttact cttgattgta acgaggattg tggaacttct gggacgcagg
 E--> 977 ggggtgggaag 3660
 W--> 978 ccctcaaata ttggtggaat ctctacagt attggagtca ggaactaaag aa-
 E--> 979 tagtgctg 3720
 W--> 980 ttaacttgct caatgccaca gccatagcag tagctgaggg gacagatagg gttata-
 E--> 981 gaag 3780
 E--> 982 tattacaagc agcttataga gctattcgcc acatacctag aagaataaga
 E--> 983 cagggtcttg 3840
 E--> 984 aaaggatttt gctataagat ggggtggcaag tgggtcaaaa gtagtgat
 E--> 985 tggatggcct 3900
 W--> 986 gctgtaaggg aaagaatgag acgagctgag ccagcagcag atgggggtggg agcag-
 E--> 987 tatct 3960
 W--> 988 cgagatctag actagaacta gcttcgatcc agacatgata agatacattg at-
 E--> 989 gaggtttg 4020
 E--> 990 acaaaccaca actagaatgc agtgaaaaaa atgctttatt tgtgaaattt
 E--> 991 gtgatgctat 4080
 W--> 992 tgctttattt gtaaccatta taagctgcaa taaacaagtt aacaacaaca attgcatt-
 E--> 993 ca 4140
 W--> 994 ttttatgttt cagggttcagg gggagggtgtg ggagggtttt taaagcaagt aa-
 E--> 995 aacctcta 4200
 W--> 996 caaatgtggt atggctgatt atgacctgc ctgcgcgctt tcggtgatga cggtgaa-
 E--> 997 aac 4260
 E--> 998 ctctgacaca tgcagctccc ggagacggtc acagcttgct tgtaagcgga
 E--> 999 tgccgggagc 4320
 W--> 1000 agacaagccc gtcagggcgc gtcagcgggt gttggcgggt gtcggggcgc agccat-
 E--> 1001 gacc 4380
 W--> 1002 cagtcacgta gcgatagcgg agtggtatact ggcttaacta tgcggcatca gagca-
 E--> 1003 gattg 4440
 E--> 1004 tactgagagt gcaccatatg tcgggcccgc ttgctggcgt tttccatag
 E--> 1005 gctccgcccc 4500
 W--> 1006 cctgacgagc atcacaaaaa tcgacgctca agtcagagggt ggcgaaaccc gacaggac-
 E--> 1007 ta 4560
 E--> 1008 taaagatacc aggcgtttcc ccctggaagc tccctcgtgc gctctcctgt
 E--> 1009 tccgacctg 4620
 W--> 1010 ccgcttaccg gatacctgct cgcctttctc ccttcgggaa gcgtggcgt ttctca-
 E--> 1011 tagc 4680
 E--> 1012 tcacgtgta ggtatctcag ttcgggtgtag gtcgttcgct ccaagctggg

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E--> 1013 ctgtgtgcac 4740
 E--> 1014 gaaccccccg ttcagccccga ccgctgcgcc ttatccggta actatcgtct
 E--> 1015 tgagtccaac 4800
 W--> 1016 ccggttaagac acgacttata gccactggca gcagccactg gtaacaggat tagca-
 E--> 1017 gagcg 4860
 W--> 1018 aggtatgtag gcggtgctac agagttcttg aagtgggtggc ctaactacgg ctacacta-
 E--> 1019 ga 4920
 W--> 1020 aggacagtat ttggtatctg cgctctgctg aagccagtta ccttcggaaa aa-
 E--> 1021 gaggttggt 4980
 W--> 1022 agctcttgat ccggcaaaca aaccaccgct ggtagcgggtg gtttttttgt ttgcaag-
 E--> 1023 cag 5040
 E--> 1024 cagattacgc gcagaaaaaa aggatctcaa gaagatcctt tgatcttttc
 E--> 1025 tacggggtct 5100
 W--> 1026 gacgtcagt ggaacgaaaa ctacagttaa gggatttttg tcatgagatt atcaa-
 E--> 1027 aaagg 5160
 W--> 1028 atcttcacct agatcctttt aaattaaaaa tgaagtttta aatcaatcta aagtata-
 E--> 1029 tat 5220
 E--> 1030 gagtaacctt ggtctgacag ttaccaatgc ttaatcagt aggcacctat
 E--> 1031 ctacgcgac 5280
 W--> 1032 tgtctatttc gttcatccat agttgcctga ctccccgtcg tgtagataac tacga-
 E--> 1033 tacgg 5340
 E--> 1034 gagggettac catctggccc cagtgtctga atgataccgc gagaccacg
 E--> 1035 ctacccggt 5400
 E--> 1036 ccagatttat cagcaataaa ccagccagcc ggaagggccg agcgcagaag
 E--> 1037 tggctctgca 5460
 W--> 1038 actttatccg cctccatcca gtctattaat tgttgccggg aagctagagt aag-
 E--> 1039 tagttcg 5520
 E--> 1040 ccagtttaata gtttgcgcaa cgttgttgcc attgtctacag gcacgtggt
 E--> 1041 gtcacgtcg 5580
 W--> 1042 tcgtttggta tggcttcatt cagctccggt tcccaacgat caaggcgagt tacat-
 E--> 1043 gatcc 5640
 W--> 1044 cccatgttgt gcaaaaaagc ggtagctcc ttcgggtctc cgatcgttgt cagaag-
 E--> 1045 taag 5700
 W--> 1046 ttggccgcag tggttatcact catgggtatg gcagcactgc ataattctct tactgt-
 E--> 1047 catg 5760
 W--> 1048 ccatccgtaa gatgcttttc tgtgactggt gagtactcaa ccaagtcatt ctgagaa-
 E--> 1049 tag 5820
 W--> 1050 tgtatgcggc gaccgagttg ctcttgcccc gcgtcaatac gggataatac cgcgcca-
 E--> 1051 cat 5880
 W--> 1052 agcagaactt taaaagtgt catcattgga aaacgttctt cggggcgaaa actct-
 E--> 1053 caagg 5940
 W--> 1054 atcttaccgc tgttgagatc cagttcgatg taaccactc gtgcacccaa ctgatctt-
 E--> 1055 ca 6000
 W--> 1056 gcacttttta ctttcaccag cgtttctggg tgagcaaaaa caggaaggca aa-
 E--> 1057 atgccgca 6060
 W--> 1058 aaaaagggaa taagggcgac acggaaatgt tgaatactca tactcttct ttttcaa-
 E--> 1059 tat 6120
 W--> 1060 tattgaagca tttatcaggg ttattgtctc atgagcggat acatatttga atgtatt-
 E--> 1061 tag 6180

same

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E--> 1062 aaaaataaac aaataggggt tccgcgcaca tttcccgaa aagtgccac
E--> 1063 6229
1066 <210> SEQ ID NO: 11
1067 <211> LENGTH: 860
1068 <212> TYPE: DNA
1069 <213> ORGANISM: Human immunodeficiency virus
1071 <220> FEATURE:
1072 <221> NAME/KEY: misc_feature
1073 <222> LOCATION: (1)..(860)
1074 <223> OTHER INFORMATION: PI-932 original sequence V1-V2-V3-loop
1076 <400> SEQUENCE: 11
W--> 1077 tgtgtaccca cagaccccaa cccacaaaag gtagtattgg aaaatgtgac agaa-
E--> 1078 aatttt 60
E--> 1079 aacatgtgga aaaatgacat ggtagaacag atgcatgagg atataatcaa
E--> 1080 tttatgggat 120
W--> 1081 caaagcctaa agccatgtgt aaaactaacc ccactctgtg ttactttaaa ttgcact-
E--> 1082 gat 180
W--> 1083 gctgatttaa attgcaataa tactgattta aattgcacta agctaattt ggggaa-
E--> 1084 aaat 240
W--> 1085 actcataaca atactattag tgggaaaata atagagaaag tagaaataaa aa-
E--> 1086 actgctct 300
W--> 1087 ttcaagggtca ccacaggcat aagggataag atgcaaaaag aatatgcact tttgaa-
E--> 1088 taaa 360
W--> 1089 cttgatatag taccaataga taatgataag aataatacta actttatatt ga-
E--> 1090 taagttgt 420
W--> 1091 aacacctga ccattacaca ggctgtcca aaggtatcct ttgagccaat tcccata-
E--> 1092 cat 480
E--> 1093 ttttgtgccc cggtgtgtt tgcgattcta aagtgtaatg aaaagagtta
E--> 1094 cagtggaaaa 540
W--> 1095 ggaccatgta aaaatgtcag cacagtacaa tgtacacatg gaattaggcc agtagtgt-
E--> 1096 ca 600
W--> 1097 actcaactgc tgttgaatgg cagtctagca gaaaaagaag tagtaattag atctga-
E--> 1098 gaat 660
W--> 1099 ttcacagaca atgctaaaac cataatagta cagctgaagg aatctgtaaa cat-
E--> 1100 tactttgt 720
W--> 1101 ataagacccc acaacactgt aacagacagg atacatatag ggccagggag atcattt-
E--> 1102 cat 780
W--> 1103 acaacaagaa aaataaaagg agatataaga caagcacatt gtagccttag gagaa-
E--> 1104 aagat 840
E--> 1105 tggaataaca ctttacaaga
E--> 1106 860
1109 <210> SEQ ID NO: 12
1110 <211> LENGTH: 870
1111 <212> TYPE: DNA
1112 <213> ORGANISM: Artificial Sequence
1114 <220> FEATURE:
1115 <223> OTHER INFORMATION: Description of the artificial sequence: PI-932
1116 gene cassette, comprising the cleavage sites for
1117 restriction enzymes BspT1, PstI, BclI, EcoRI,

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1118 BglII, PvuII, XbaII, NheI
1120 <400> SEQUENCE: 12
W--> 1121 tgtgtaccca cagaccccaa cccacaaaag gtagtattgg aaaatgtgac agaa-
E--> 1122 aatttt 60
E--> 1123 aacatgtgga aaaatgacat ggtagaacag atgcatgagg atataatcaa
E--> 1124 tttatgggat 120
W--> 1125 caaagcctta agccatgtgt aaaactaacc ccactctgtg ttactttaaa ttgcact-
E--> 1126 gat 180
W--> 1127 gctgatttaa attgcaataa tactgattta aattgcacta aagctaattt ggggaa-
E--> 1128 aaat 240
W--> 1129 actcataact gcagtattag tgggaaaata atagagaaag tagaaataaa aa-
E--> 1130 actgctct 300
W--> 1131 ttcaaggtca ccacaggcat aagggataag atgcaaaaag aatatgcact tttgaa-
E--> 1132 taaa 360
W--> 1133 cttgatatag taccaataga taatgataag aataatacta actttatatt ga-
E--> 1134 taagttgt 420
W--> 1135 aacacctcgg tgatcacaca ggcctgtcca aaggatcct ttgagccaat tcccata-
E--> 1136 cat 480
E--> 1137 ttttgtgccc cggttggttt tgcgattcta aagtgtaatg aaaagagtta
E--> 1138 cagtggaaaa 540
W--> 1139 ggaccatgta aaaatgtcag cacagtacaa tgtacacatg gaattcggcc agtagtgt-
E--> 1140 ca 600
W--> 1141 actcaactgc tgttgaatgg cagtctagca gaaaaagaag tagtaattag atctga-
E--> 1142 gaat 660
W--> 1143 ttcacagaca atgctaaaac cataatagta cagctgaagg aatctgtaaa cat-
E--> 1144 tacttgt 720
W--> 1145 ataagacccc acaacactgt aacagacagg atacatatag ggccagggag atcattt-
E--> 1146 cat 780
W--> 1147 acaacaagaa aaataaaagg agatataaga caagcacatt gtagcctttc tagaa-
E--> 1148 aagat 840
E--> 1149 tggaataaca ctttacaaga gatagctagc
E--> 1150 870

FWI

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

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Output Set: N:\CRF3\08162001\I913159.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:28 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:28 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:2 SEQ:1
L:29 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:30 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:31 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:32 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:33 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:39 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:41 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:45 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:47 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:51 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:52 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:53 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:55 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:59 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:63 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:65 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:69 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:71 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:75 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:79 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:81 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:82 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:83 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:85 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

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L:89 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:93 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:94 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:95 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:97 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:99 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:103 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:109 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:111 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:113 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:115 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:123 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:127 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:131 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:135 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:137 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:139 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:140 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:143 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:145 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:147 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:153 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6

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L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:155 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:161 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:163 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:350 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9709 Found:2943 SEQ:1
L:644 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:4 SEQ:3
M:254 Repeated in SeqNo=3
L:646 M:252 E: No. of Seq. differs, <211>LENGTH:Input:107 Found:51 SEQ:3
L:667 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:4
L:669 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
M:254 Repeated in SeqNo=4
L:683 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:5
L:697 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:6
L:711 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:7
L:725 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:8
L:748 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:9
M:254 Repeated in SeqNo=9
L:819 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2148 Found:587 SEQ:9
L:857 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:2 SEQ:10
M:254 Repeated in SeqNo=10
L:1063 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6229 Found:2504 SEQ:10
L:1078 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:6 SEQ:11
M:254 Repeated in SeqNo=11
L:1106 M:252 E: No. of Seq. differs, <211>LENGTH:Input:860 Found:197 SEQ:11
L:1122 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:6 SEQ:12
M:254 Repeated in SeqNo=12
L:1150 M:252 E: No. of Seq. differs, <211>LENGTH:Input:870 Found:207 SEQ:12